Paper Alert

Chosen by Robert Liddington[1], Christin Frederick[2], Jane Clarke[3] and Sophie Jackson[3]

A selection of interesting papers that were published in the month before our press date in major journals most likely to report significant results in structural biology, protein and RNA folding.

[1]Department of Biochemistry, University of Leicester, Leicester LE1 7RH, UK, [2]Laboratory of X-ray Crystallography, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA and [3]Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge CB2 1EW, UK.

Structure 1999, Vol 7 No 2:R37–R41

☐ Monitoring the sizes of denatured ensembles of Staphylococcal nuclease proteins: implications regarding ***m*** values, intermediates, and thermodynamics. Ilia V Baskakov and DW Bolen (1998). *Biochemistry* 37, 18010–18017.

Fluorescence and size-exclusion chromatography were used to monitor urea denaturation of wild-type staphylococcal nuclease (SN) as well as the *m*+ and *m*– mutants A69T and V66W. The rank order of *m* values of the SN proteins studied do not correspond to the rank order of denatured ensemble sizes defected by $1/K_d$ suggesting that *m* values reflect more than just surface area increases on denaturation. Fluorescence-detected urea denaturations of A69T and wt SN do not correspond with $1/K_d$-detected denaturation profiles, a result that would ordinarily mean that the transitions are non-two-state. However, this interpretation fails to recognise the rapidly changing size and thermodynamic character of the denatured ensembles of these proteins both within and outside the transition zone.
1 December 1998, *Biochemistry*

☐ Characterization of the transthyretin acid denaturation pathways by analytical ultracentrifugation: implications for wild-type, V30M, and L55P amyloid fibril formation. Hilal A Lashuel, Zhihong Lai and Jeffery W Kelly (1998). *Biochemistry* 37, 17851–17864.

Analytical centrifugation methods were used to further characterize the acid denaturation pathways of wild-type, V30M, and L55P transthyretin (TTR) that generate intermediates leading to amyloid fibril formation. This study establishes the key role of the monomeric amyloidogenic intermediate and its self-assembly into a ladder of quaternary structural intermediates for the formation of wild-type, V30M, and L55P transthyretin amyloid fibrils.
1 December 1998, *Biochemistry*

■ Structure of an IκBα/NF-κB complex. Marc D Jacobs and Stephen C Harrison (1998). *Cell* 95, 749–758.

The inhibitory protein, IκBα, sequesters the transcription factor, NF-κB, as an inactive complex in the cytoplasm. The crystal structure of the IκBα ankyrin repeat domain, bound to a partially truncated NF-κB heterodimer (p50–p65), has been determined. It shows a stack of six IκBα ankyrin repeats facing the C-terminal domains of the NF-κB Rel homology regions. Contacts occur in discontinuous patches, suggesting a combinatorial quality for ankyrin repeat specificity. The orientation of IκBα in the complex places its N- and C-terminal regions in appropriate locations for their known regulatory functions. (Similar results are reported in the same issue of *Cell* by Huxford, T., Huang, D.-B., Malek, S. & Ghosh, G. (1998) *Cell* **95**, 759–770.)
11 December 1998, *Cell*

☐ Transmembrane signaling across the ligand-gated FhuA receptor: crystal structures of free and ferrichrome-bound states reveal allosteric changes. Kaspar P Locher, Bernard Rees, Ralf Koebnik, André Mitschler, Luc Moulinier, Jurg P Rosenbusch and Dino Moras (1998). *Cell* 95, 771–778.

FhuA protein facilitates ligand-gated transport of ferrichrome-bound iron across *Escherichia coli* outer membranes. X-ray analysis reveals two distinct conformations in the presence and absence of ferrichrome. The monomeric protein consists of a hollow, 22-stranded, antiparallel β barrel (residues 160–714), which is obstructed by a plug (residues 19–159). The binding site of ferrichrome, an aromatic pocket near the cell surface, undergoes minor changes upon association with the ligand. These are propagated and amplified across the plug, eventually resulting in substantially different protein conformations at the periplasmic face.
11 December 1998, *Cell*

☐ The structural basis of estrogen receptor/coactivator recognition and the antagonism of this interaction by tamoxifen. Andrew K Shiau, Danielle Barstad, Paula M Loria, Lin Cheng, Peter J Kushner, David A Agard and Geoffrey L Greene (1998). *Cell* 95, 927–937.

The authors report the crystal structure of the human estrogen receptor α (hERα) ligand-binding domain (LBD) bound to both the agonist diethylstilbestrol (DES) and a peptide derived from the NR box II region of the coactivator GRIP1 and the crystal structure of the hERα LBD bound to the

■ See the Minireview article by Patrick Cramer and Christoph W Müller in the 15 January issue of *Structure* with *Folding & Design* (volume 7:R1–R6).

selective antagonist 4-hydroxytamoxifen (OHT). In the DES–LBD-peptide complex, the peptide binds as a short α helix to a hydrophobic groove on the surface of the LBD. In the OHT–LBD complex, helix 12 occludes the coactivator recognition groove by mimicking the interactions of the NR box peptide with the LBD. These structures reveal the two distinct mechanisms by which structural features of OHT promote this 'autoinhibitory' helix 12 conformation.
23 December 1998, *Cell*

☐ Crystal structure of constitutive endothelial nitric oxide synthase: a paradigm for pterin function involving a novel metal center. CS Raman, Huiying Li, Pavel Martásek, Vladimir Král, Bettie Sue S Masters and Thomas L Poulos (1998). *Cell* 95, 939–950.
Nitric oxide, a key signaling molecule, is produced by a family of enzymes collectively called nitric oxide synthases (NOS). The authors report the crystal structure of the heme domain of endothelial NOS in tetrahydrobiopterin (H_4B)-free and -bound forms. In both structures a zinc ion is tetrahedrally coordinated to pairs of symmetry-related cysteine residues at the dimer interface. The unexpected recognition of the substrate, L-arginine, at the H_4B site indicates that this site is poised to stabilize a positively charged pterin ring and suggests a model involving a cationic pterin radical in the catalytic cycle.
23 December 1998, *Cell*

☐ Crystal structure of the human high-affinity IgE receptor. Scott C Garman, Jean-Pierre Kinet and Theodore S Jardetzky (1998). *Cell* 95, 951–961.
Allergic responses result from the activation of mast cells by the human high-affinity IgE receptor. The initiation of a response requires the binding of IgE to its high-affinity receptor. The authors have solved the crystal structure of the antibody-binding domains of the human IgE receptor. The structure reveals a highly bent arrangement of immunoglobulin domains that form an extended convex surface of interaction with IgE. A prominent loop that confers specificity for IgE molecules extends from the receptor surface near an unusual arrangement of four exposed tryptophans.
23 December 1998, *Cell*

☐ Crystal structure of the ***Oxytricha nova*** telomere end binding protein complexed with single strand DNA. Martin P Horvath, Viloya L Schweiker, Joanne M Bevilacqua, James A Ruggles and Steve C Schultz (1998). *Cell* 95, 963–974.
Telomeres are specialized protein–DNA complexes that protect chromosome termini from degradation and recombination. The authors have determined the crystal structure of the two-subunit *Oxytricha nova* telomere end binding protein (OnTEBP) complexed with single strand telomeric DNA. This structure provides a molecular description of how the two subunits of OnTEBP recognize and bind ssDNA to form a sequence-specific, telomeric nucleoprotein complex that caps the very 3′ ends of chromosomes.
23 December 1998, *Cell*

☐ The structure of plasmid-encoded transcriptional repressor CopG unliganded and bound to its operator. F Xavier Gomis-Rüth, Maria Solà, Paloma Acebo, Antonio Párraga, Alicia Guasch, Ramón Eritja, Ana González, Manuel Espinosa, Gloria del Solar and Miquel Coll (1998). *EMBO J.* 17, 7404–7415.
The structure of the 45 amino acid transcriptional repressor, CopG, has been solved unliganded and bound to its target operator DNA. The protein has a homodimeric ribbon-helix-helix arrangement. In the complex structure, one protein tetramer binds at one face of a 19 base pair oligonucleotide, containing the pseudosymmetric element, with two β ribbons inserted into the major groove. The protein dimer displays topological similarity to Arc and MetJ repressors but the functional tetramer has a unique structure.
15 December 1998, *The EMBO Journal*

☐ Structure of the 3′-hairpin of the TYMV pseudoknot: preformation in RNA folding. Michaël H Kolk, Marinette van der Graaf, Carel TM Fransen, Sybren S Wijmenga, Cornelis WA Pleij, Hans A Heus and Cornelis W Hilbers (1998). *EMBO J.* 17, 7498–7504.
The solution structure of an RNA hairpin present in the pseudoknot, which is found at the 3′-terminus of turnip yellow mosaic virus (TYMV) genomic RNA, has been solved by NMR spectroscopy. The loop, which contains the sequence 5′-GGGUCA-3′, was found to be highly structured and, contrary to expectations, does not attain its stability through GA or GC base pair formation but by triple interactions between the tilted adenosine and the minor groove sides of the first two guanosines. A very similar conformation was found for the cognate pseudoknot, implying that the 3′-hairpin is preformed for folding into a pseudoknotted structure.
15 December 1998, *The EMBO Journal*

☐ Molecular basis of double-stranded RNA–protein interactions: structure of a dsRNA-binding domain complexed with dsRNA. Jodi M Ryter and Steve C Schultz (1998). *EMBO J.* 17, 7505–7513.
A large class of proteins that bind dsRNA utilize an ~70 amino acid motif known as the dsRNA-binding domain (dsRBD). The crystal structure of the second dsRBD of *Xenopus laevis* RNA-binding protein A complexed with dsRNA shows that the protein spans 16 base pairs of dsRNA, interacting with two successive minor grooves and across the intervening major groove on one face of a primarily A-form RNA helix. The nature of these interactions explains dsRBD specificity for dsRNA (over ssRNA or dsDNA) and the apparent lack of sequence specificity.
15 December 1998, *The EMBO Journal*

● Crystal structures of open and closed forms of binary and ternary complexes of the large fragment of ***Thermus aquaticus*** DNA polymerase I: structural basis for nucleotide incorporation. Ying Li, Sergey Korolev and Gabriel Waksman (1998). *EMBO J.* 17, 7514–7525.

The authors present crystal structures of one binary and two ternary complexes of the large fragment of *Thermus aquaticus* DNA polymerase I (Klentaq1) with a primer–template DNA and dideoxycytidine triphosphate. One ternary complex structure differs markedly from the other two structures by a large reorientation of the tip of the fingers domain, and represents the ternary polymerase complex caught in the act of incorporating a nucleotide. These structures provide the first direct evidence in DNA polymerase I enzymes of a large conformational change responsible for assembling an active ternary complex.

15 December 1998, *The EMBO Journal*

□ Crystal structure of methionyl-tRNA$_f^{Met}$ transformylase complexed with the initiator formyl-methionyl-tRNA$_f^{Met}$. Emmanuelle Schmitt, Michel Panvert, Sylvain Blanquet and Yves Mechulam (1998). *EMBO J.* 17, 6819–6826.

In the crystal structure of *Escherichia coli* methionyl-tRNA$_f^{Met}$, transformylase complexed with formyl-methionyl-tRNA$_f^{Met}$ the methionyl-tRNA$_f^{Met}$ formyltransferase fills in the inside of the L-shaped tRNA molecule on the D stem side. The C1–A72 mismatch characteristic of the initiator tRNA is split and the 3′ arm bends inside the active centre. This recognition mechanism is markedly distinct from that of elongation factor Tu.

15 December 1998, *The EMBO Journal*

□ A protein folding intermediate of ribonuclease T_1 characterised at high resolution by 1D and 2D real-time NMR spectroscopy. Jochen Balbach, Clemens Steegborn, Thomas Schindler and Franz X Schmid (1998). *J. Mol. Biol.* 285, 829–842.

The major intermediate on the folding pathway of ribonuclease T_1 was characterized by a novel NMR method. Real-time 2D-NOESY experiments were employed in conjunction with a new assignment strategy which generates positive and negative signal intensity for native and non-native NOE cross-peaks, respectively. The major intermediate folds slowly at 10°C due to the presence of a non-native *trans* proline bond. Although some regions of the intermediate are found to have native-like structure, there are significant regions with non-native structure.

15 January 1999, *Journal of Molecular Biology*

□ High populations of non-native structure in the denatured state are compatible with the formation of the native folded state. Fransisco J Blanco, Luis Serrano and Julie Forman-Kay (1998). *J. Mol. Biol* 284, 1153–1164.

The denatured state of the all-β spectrin SH3 domain was characterised under mildly acidic conditions by NMR spectroscopy. Wild type and a mutant, in which the N-terminal region was redesigned to form helical structure, were studied. Whereas wild type shows little evidence of residual structure in the denatured state, the mutant has ~50% helical structure. Comparison with a small peptide corresponding to this region shows that structure is stabilised by long-range interactions. Despite the helical-forming tendencies of this engineered region there is little effect on the folding or final state of this protein.

11 December 1998, *Journal of Molecular Biology*

□ Structure of the transition state in the folding process of human procarboxypeptidase A2 activation domain. Virtudes Villegas, Jose C Martinez, Francesco X Aviles and Luis Serrano (1998). *J. Mol. Biol.* 283, 1027–1036.

Protein engineering techniques and φ value analysis were used to characterise the transition state for folding of this 81-residue, α/β protein. Twenty single point mutations report on the formation of secondary and tertiary structure in the transition state which is found to be relatively compact, with a hydrophobic core that is in the process of being consolidated in the transition state. Interestingly, although α helix 1 has a tendency to form structure in the denatured state it is not formed in the transition state. Thus, residual structure in unfolded states does not always influence the folding pathway.

13 November 1998, *Journal of Molecular Biology*

□ Crystal structure of the ATP-binding subunit of an ABC transporter. Li-Wei Hung, Iris Xiaoyan Wang, Kishiko Nikaido, Pei-Qi Liu Giovanna Ferro-Luzzi Ames and Sung-Hou Kim (1998). *Nature* 396, 703–707.

ABC transporters are proteins responsible for the translocation of a variety of compounds across membranes of both prokaryotes and eukaryotes. The crystal structure of HisP, the ATP-binding subunit of the histidine permease, which is an ABC transporter from *Salmonella typhimurium*, provides a basis for understanding properties of a large family of medically important proteins.

17 December 1998, *Nature*

□ Crystal structure of the ligand-binding domain of the receptor tyrosine kinase EphB2. Juha-Pekka Himanen, Mark Henkemeyer and Dimitar B Nikolov (1998). *Nature* 396, 486–491.

The Eph receptors are receptor tyrosine kinases (RTKs) that are important in contact-mediated axon guidance, axon fasciculation and cell migration. The crystal structure of the N-terminal ligand-binding domain of the EphB2 receptor reveals a compact jellyroll β sandwich composed of 11 antiparallel β strands. Using structure-based mutagenesis, an extended loop has been identified that is important for ligand binding and class specificity.

3 December 1998, *Nature*

● See the Minireview article by Sylvie Doublié, Michael R Sawaya and Tom Ellenberger in this issue of *Structure* with *Folding & Design* (volume 7:R31–R35).

☐ Upper limit of the time scale for diffusion and chain collapse in chymotrypsin inhibitor 2. Andreas G Ladurner and Alan R Fersht (1998). *Nat. Struct. Biol.* 6, 28–31.
The rates of folding of wild-type chymotrypsin inhibitor 2 (CI2) ($t_{½}$ = 12 ms) and of faster ($t_{½}$ = 2 ms) and slower ($t_{½}$ = 350 ms) folding mutants are accelerated in parallel by increasing concentrations of sucrose, despite the increases in viscosity. At a viscosity 26 times that of water, the folding rate constant of wild-type CI2 is accelerated fourfold (t½ = 2.7 ms). From this, the authors estimate that the diffusional chain collapse in CI2 occurs in less than 100 μs in water, and is not rate-determining in folding.
January 1999, *Nature Structural Biology*

☐ Crystal structure of a plant catechol oxidase containing a dicopper center. Thomas Klabunde, Christoph Eicken, James C Sacchettini and Bernt Krebs (1998). *Nat. Struct. Biol.* 5, 1084–1090.
Catechol oxidases are ubiquitous plant enzymes containing a dinuclear copper center. In the wound-response mechanism of the plant they catalyze the oxidation of a broad range of *ortho*-diphenols to the corresponding *o*-quinones coupled with the reduction of oxygen to water. The crystal structures of the enzyme from sweet potato in the resting dicupric Cu(II)-Cu(II) state, the reduced dicuprous Cu(I)-Cu(I) form, and in complex with the inhibitor phenylthiourea were analyzed. The catalytic copper center is accommodated in a central four-helix bundle located in a hydrophobic pocket close to the surface. Both metal-binding sites are composed of three histidine ligands.
December 1998, *Nature Structural Biology*

☐ Structure and mutagenesis of the Dbl homology domain. Behzad Aghazadeh, Kejin Zhu, Terrance J Kubiseski, Grace A Liu, Tony Pawson, Yi Zheng and Michael K Rosen (1998). *Nat. Struct. Biol.* 5, 1098–1107.
Guanine nucleotide exchange factors in the Dbl family activate Rho GTPases by accelerating dissociation of bound GDP. Dbl proteins possess an ~200-residue catalytic Dbl-homology (DH) domain, that is arranged in tandem with a C-terminal pleckstrin homology (PH) domain. The authors report the solution structure of the DH domain of human PAK-interacting exchange protein (βPIX). The domain is composed of 11 α helices that form a flattened, elongated bundle. The GTPase interaction site is formed by three conserved helices near the center of one face of the domain.
December 1998, *Nature Structural Biology*

☐ Structure of a human DNA repair protein UBA domain that interacts with HIV-1 Vpr. Thorsten Dieckmann, Elizabeth S Withers-Ward, Mark A Jarosinski, Cuan-Fa Liu, Irvin SY Chen and Juli Feigon (1998). *Nat. Struct. Biol.* 5, 1042–1047.
The HIV-1 protein Vpr interacts specifically with the second UBA (ubiquitin-associated) domain found in the DNA repair protein HHR23A. The authors present the three-dimensional structure of the UBA domain, determined by NMR spectroscopy. The protein domain forms a compact three-helix bundle. One side of the protein has a hydrophobic surface that is the most likely Vpr target site.
December 1998, *Nature Structural Biology*

☐ HIV-1 A-rich RNA loop mimics the tRNA anticodon structure. Elisabetta Viani Puglisi and Joseph D Puglisi (1998). *Nat. Struct. Biol.* 5, 1033–1036.
Interaction of HIV-1 genomic RNA and human $tRNA^{Lys}$ initiates viral reverse transcription. An adenosine-rich (A-rich) loop in HIV RNA mediates complex formation between tRNA and viral RNA. The authors have determined the structure of an A-rich loop oligonucleotide using NMR spectroscopy. The loop structure is stabilized by a noncanonical G–A pair and a U-turn motif, which leads to stacking of the conserved adenosines. The structure has similarity to the tRNA anticodon structure, and suggests possible mechanisms for its role in initiation of reverse transcription.
December 1998, *Nature Structural Biology*

☐ Maturation of the tyrosine kinase c-src as a kinase and as a substrate depends on the molecular chaperone hsp90. Yang Xu, Mike A Singer and Susan Lindquist (1999). *Proc. Natl Acad. Sci. USA* 96, 109–114.
A new strain of *Saccharomyces cerevisiae*, which expresses approximately one-twentieth of the normal level of hsp90, was used to address the question of whether hsp90 was required for the correct maturation of the normal cellular tyrosine kinase c-src. In contrast to its viral counterpart v-src, c-src does not interact strongly with hsp90. Experiments showed that hsp90 is essential for the correct maturation of c-src. Mapping experiments indicate that it is the C-terminal region of v-src that is responsible for the difference.
5 January 1999, *Proceedings of the National Academy of Science USA*

☐ Structure of a biological oxygen sensor: a new mechanism for heme-driven signal transduction. Weimin Gong, Bing Hao, Sheref S Mansy, Gonzalo Gonzalez, Marie A Gilles-Gonzalez and Michael K Chan (1998). *Proc. Natl Acad. Sci. USA* 95, 15177–15182.
The FixL proteins are biological oxygen sensors that restrict the expression of specific genes to hypoxic conditions. FixL's oxygen-detecting domain is a heme-binding region that controls the activity of an attached histidine kinase. Comparison of the structures of two forms of the *Bradyrhizobium japonicum* FixL heme domain, one in the 'on' state without bound ligand and one in the 'off' state with bound cyanide, reveals a mechanism of regulation by a heme that is distinct from the classical hemoglobin models.
22 December 1998, *Proceedings of the National Academy of Science USA*

☐ Structure-based assignment of the biochemical function of a hypothetical protein: a test case of structural genomics. Thomas I Zarembinski, Li-Wei Hung, Hans-Joachim Mueller-Dieckmann, Kyeong-Kyu Kim, Hisao Yokota, Rosalind Kim and Sung-Hou Kim (1998). *Proc. Natl Acad. Sci. USA* 95, 15189–15193.

The authors report the crystal structure of a small protein of unknown function, MJ0577, from a hyperthermophile, *Methanococcus jannaschii*. The structure contains a bound ATP, suggesting MJ0577 is an ATPase or an ATP-mediated molecular switch, which was confirmed by biochemical experiments. Furthermore, the structure reveals different ATP-binding motifs that are shared among many homologous hypothetical proteins in this family. This result indicates that structure-based assignment of molecular function is a viable approach for the large-scale biochemical assignment of proteins and for discovering new motifs, a basic premise of structural genomics.

22 December 1998, *Proceedings of the National Academy of Science USA*

☐ Structural code for DNA recognition revealed in crystal structures of papillomavirus E2-DNA targets. Haim Rozenberg, Dov Rabinovich, Felix Frolow, Rashmi S Hegde and Zippora Shakked (1998). *Proc. Natl Acad. Sci. USA* 95, 15194–15199.

Transcriptional regulation in papillomaviruses depends on sequence-specific binding of the regulatory protein E2 to several sites in the viral genome. Crystal structures of bovine papillomavirus E2 DNA targets reveal a conformational variant of B-DNA characterized by a roll-induced writhe and helical repeat of 10.5 base pairs per turn. A comparison between the free and the protein-bound DNA demonstrates that the structure deformability of the DNA is critical for sequence-specific protein–DNA recognition and hence for gene-regulatory signals in the viral system.

22 December 1998, *Proceedings of the National Academy of Science USA*

☐ High-resolution NMR of encapsulated proteins dissolved in low-viscosity fluids. A Joshua Wand, Mark R Ehrhardt and Peter F Flynn (1998). *Proc. Natl Acad. Sci. USA* 95, 15299–15302.

The majority of known proteins are too large to be comprehensively examined by solution NMR methods, primarily because they tumble too slowly in solution. The authors introduce an approach to making the NMR relaxation properties of large proteins amenable to modern solution NMR techniques. The encapsulation of a protein in a reverse micelle dissolved in a low-viscosity fluid allows it to tumble as fast as a much smaller protein. The approach is demonstrated with the protein ubiquitin.

22 December 1998, *Proceedings of the National Academy of Science USA*

☐ X-ray crystal structure of the Fe-only hydrogenase (CpI) from ***Clostridium pasteurianum*** to 1.8 Å resolution. John W Peters, William N Lanzilotta, Brian J Lemon and Lance C Seefeldt (1998). *Science* 282, 1853–1858.

The crystal structure of the monomeric iron-containing hydrogenase (CpI) from *Clostridium pasteurianum* is described. CpI, an enzyme that catalyzes the two-electron reduction of two protons to yield dihydrogen, was found to contain 20 gram atoms of iron per mole of protein, arranged into five distinct [Fe–S] clusters. The probable active-site cluster, previously termed the H cluster, was found to be an arrangement of six iron atoms existing as a [4Fe–4S] cubane subcluster covalently bridged by a cysteinate thiol to a [2Fe] subcluster.

4 December 1998, *Science*

☐ Crystal structure of quinolinic acid phosphoribosyltransferase from ***Mycobacterium tuberculosis***: a potential TB drug target. Vivek Sharma, Charles Grubmeyer and James C Sacchettini (1998). *Structure* 6, 1587–1599.

The crystal structure of the *Mycobacterium tuberculosis* quinolinic acid phosphoribosyltransferase (QAPRTase) has been determined in complex with substrate, product and substrate analogs. QAPRTase, a key enzyme in the *de novo* biosynthesis of NAD, provides an attractive target for designing novel antitubercular drugs. The enzyme is the only known representative of the type II PRTase fold, an unusual α/β barrel. The active site bears little resemblance to the better known type I enzymes.

15 December 1998, *Structure*

☐ The crystal structure of pneumococcal surface antigen PsaA reveals a metal-binding site and a novel structure for a putative ABC-type binding protein. Michael C Lawrence, Patricia A Pilling, V Chandana Epa, Anne M Berry, A David Ogunniyi and James C Paton (1998). *Structure* 6, 1553–1561.

The surface protein PsaA of the pathogenic bacterium *Streptococcus pneumoniae* is required for its virulence. The crystal structure of PsaA consists of two $(\beta/\alpha)_4$ domains linked together by a single helix. The structure is fundamentally different from that of other ABC-type binding proteins in that PsaA lacks the characteristic 'hinge peptides' involved in conformational change upon solute uptake and release.

15 December 1998, *Structure*